

WEST Search History

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DATE: Wednesday, August 16, 2006

Hide?	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
	<i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>		
<input type="checkbox"/>	L8	L7 not l6	55
<input type="checkbox"/>	L7	L3 and kidney	189
<input type="checkbox"/>	L6	l2 and (autoimmune or lupus or sle)	152
<input type="checkbox"/>	L5	L4 and l1	1
<input type="checkbox"/>	L4	L2 same (autoimmune or lupus or sle)	1
<input type="checkbox"/>	L3	l2 and (array or microarray or profile)	227
<input type="checkbox"/>	L2	L1 same (expression or mRNA)	308
<input type="checkbox"/>	L1	SFRP1 or FRP or SARP2 or (secreted adj (apoptosis or frizzled) adj related adj protein)	18257

END OF SEARCH HISTORY

SYSTEM:OS - DIALOG OneSearch

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(c) 2006 The HW Wilson Co.
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- File 155:MEDLINE(R) 1950-2006/Aug 15
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- File 172:EMBASE Alert 2006/Aug 16
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- File 266:FEDRIP 2005/Dec
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- File 315:ChemEng & Biotec Abs 1970-2006/Jul
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- File 358:Current BioTech Abs 1983-2006/Jan
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- File 370:Science 1996-1999/Jul W3
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(c) 2006 American Chemical Society
- *File 399: Use is subject to the terms of your user/customer agreement.
IPCR/8 classification codes now searchable as IC=. See HELP NEWSIPCR.

Set Items Description

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? s SFRP1 or (secreted (w) frizzle$ (w) related (w) protein) or SARP2 or SFRP-1
555 SFRP1
328608 SECRETED
0 FRIZZLE$
7877444 RELATED
10289834 PROTEIN
0 SECRETED(W)FRIZZLE$(W)RELATED(W)PROTEIN
41 SARP2
33 SFRP-1
S1 627 SFRP1 OR (SECRETED (W) FRIZZLE$ (W) RELATED (W) PROTEIN)
OR SARP2 OR SFRP-1
? s SFRP1 or (secreted (w) frizzled (w) related (w) protein) or SARP2 or SFRP-1
Processing
Processed 20 of 26 files ...
Completed processing all files
555 SFRP1
328608 SECRETED
6916 FRIZZLED
7877444 RELATED
10289834 PROTEIN
1027 SECRETED(W)FRIZZLED(W)RELATED(W)PROTEIN
41 SARP2
33 SFRP-1
S2 1377 SFRP1 OR (SECRETED (W) FRIZZLED (W) RELATED (W) PROTEIN)
OR SARP2 OR SFRP-1
s s2 and (autoimmune or lupus or sle or RA or rheumatoid)
1377 S2
491380 AUTOIMMUNE
271377 LUPUS
78024 SLE
617272 RA
422382 RHEUMATOID
S3 42 S2 AND (AUTOIMMUNE OR LUPUS OR SLE OR RA OR RHEUMATOID)
? rd s3
S4 17 RD S3 (unique items)
? s s2 and (expression or mRNA or profile)
1377 S2
6020558 EXPRESSION
1391965 MRNA
1135906 PROFILE
S5 1015 S2 AND (EXPRESSION OR MRNA OR PROFILE)
? s s5 and (array or microarray)
1015 S5
584443 ARRAY
164260 MICROARRAY
S6 188 S5 AND (ARRAY OR MICROARRAY)
? rd s6
S7 84 RD S6 (unique items)
? s s7 not s3
84 S7
42 S3
S8 80 S7 NOT S3t s10/6/1-38

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Run on: August 3, 2006, 10:58:55 ; Search time 24395 Seconds
 (without alignments)
 11714.738 Million cell updates/sec

Title: US-10-786-720-15
 Perfect score: 4469
 Sequence: 1 cctgcagcctccggagtcag.....taatcaatgaaaaaaaaaaaa 4469

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : GenEmbl:*
 1: gb_env:*
 2: gb_pat:*
 3: gb_ph:*
 4: gb_pl:*
 5: gb_pr:*
 6: gb_ro:*
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 8: gb_sy:*
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 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4469	100.0	4469	2	CS025753	CS025753 Sequence
2	4469	100.0	4469	2	AX236302	AX236302 Sequence
3	4469	100.0	4469	2	AX578081	AX578081 Sequence
4	4469	100.0	4469	5	AF056087	AF056087 Homo sapi
5	4356.8	97.5	4500	2	AR253209	AR253209 Sequence
6	4339.4	97.1	4482	5	BC036503	BC036503 Homo sapi
7	3935	88.1	4245	2	AR129158	AR129158 Sequence
8	3580.6	80.1	3670	2	BD135188	BD135188 Human nuc
9	3580.6	80.1	3670	2	AX017498	AX017498 Sequence
10	3504.8	78.4	3872	2	CQ850220	CQ850220 Sequence
11	3504.8	78.4	3872	5	AK127331	AK127331 Homo sapi
12	3448	77.2	171133	5	AC103846	AC103846 Homo sapi
13	3448	77.2	188270	5	AC104393	AC104393 Homo sapi

14	3081	68.9	3181	2	BD205077	BD205077 Human nuc
15	3081	68.9	3181	2	AX013686	AX013686 Sequence
16	2465.4	55.2	2602	2	AX099741	AX099741 Sequence
17	2075	46.4	2075	2	AR253206	AR253206 Sequence
18	2075	46.4	2075	2	AR361924	AR361924 Sequence
19	2075	46.4	2075	2	AR433000	AR433000 Sequence
20	2075	46.4	2075	2	AX482567	AX482567 Sequence
21	2075	46.4	2075	2	AX565707	AX565707 Sequence
22	2075	46.4	2075	2	AX597107	AX597107 Sequence
23	2075	46.4	2075	2	AX701365	AX701365 Sequence
24	2075	46.4	2075	5	AF001900	AF001900 Homo sapi
25	2062	46.1	2078	2	AR253205	AR253205 Sequence
26	1991.6	44.6	2094	5	AF017987	AF017987 Homo sapi
27	1476.6	33.0	4240	14	BTU85945	U85945 Bos taurus
28	1256.6	28.1	1308	2	BD217906	BD217906 Gene fami
29	1196.8	26.8	4375	6	BC094662	BC094662 Mus muscu
30	923.8	20.7	945	8	AY891055	AY891055 Synthetic
31	923.8	20.7	945	8	BT019677	BT019677 Synthetic
c 32	906.4	20.3	197427	12	AC182062	AC182062 Bos tauru
33	899.8	20.1	942	2	AR361925	AR361925 Sequence
34	899.8	20.1	942	2	AX482568	AX482568 Sequence
35	896.8	20.1	1017	2	AR361926	AR361926 Sequence
36	896.2	20.1	1340	6	BC024495	BC024495 Mus muscu
37	886.4	19.8	2659	6	MMU88566	U88566 Mus musculu
38	828.2	18.5	155691	5	AC016868	AC016868 Homo sapi
39	776.2	17.4	2124	2	AR253208	AR253208 Sequence
40	703.6	15.7	3065	11	GGA404652	AJ404652 Gallus ga
41	684.2	15.3	804	2	AR361929	AR361929 Sequence
42	621.2	13.9	741	2	AR361928	AR361928 Sequence
43	609.6	13.6	1146	2	AX565729	AX565729 Sequence
44	609.6	13.6	1146	2	AX597129	AX597129 Sequence
45	609.6	13.6	1146	2	AX701375	AX701375 Sequence
46	609.4	13.6	770	5	HSA325301	AJ325301 Homo sapi
47	609	13.6	726	7	BV208829	BV208829 SFRP1_189
c 48	588	13.2	241809	6	AC139848	AC139848 Mus muscu
c 49	536	12.0	184377	6	AC147247	AC147247 Mus muscu
c 50	527	11.8	548	2	AR280573	AR280573 Sequence

Run on: August 3, 2006, 10:56:23 ; Search time 2549 Seconds
 (without alignments)
 12224.001 Million cell updates/sec

Title: US-10-786-720-15
 Perfect score: 4469
 Sequence: 1 cctgcagcctccggagtcag.....taatcaatgaaaaaaaaaaaa 4469

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : N_Geneseq_8:*
 1: geneseqn1980s:*
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 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
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 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		% Query					
Result	No.	Score	Match Length	DB	ID	Description	
	1	4469	100.0	4469	4	AAS12954	
	2	4469	100.0	4469	6	ABT10165	
	3	4469	100.0	4469	8	ABZ34845	
	4	4469	100.0	4469	12	ADP21417	
	5	4469	100.0	4469	13	ADR24996	
	6	4469	100.0	4469	13	ADR99015	
	7	4469	100.0	4469	13	AEA64538	
	8	4469	100.0	4469	14	ADV44809	
	9	4469	100.0	4469	14	ADX58915	
c	10	4439.8	99.3	4608	14	AED73309	
	11	4393.4	98.3	4462	8	ABX77526	
	12	4355.4	97.5	4616	4	AAH72901	
	13	4355.2	97.5	4497	2	AAV84395	

	14	4335.4	97.0	4451	8	ABZ82226	Abz82226 Human sFR
	15	3935	88.1	4245	4	AAF80506	Aaf80506 Cell prol
	16	3580.6	80.1	3670	2	AAZ33577	Aaz33577 Human bre
	17	3504.8	78.4	3872	13	ADR07183	Adr07183 Full leng
	18	3102.6	69.4	3215	3	AAC77657	Aac77657 Human can
	19	3090.4	69.2	3216	2	AAZ33608	Aaz33608 Human bre
	20	3069	68.7	3180	2	AAZ42127	Aaz42127 Human nor
	21	2465.4	55.2	2602	12	ADP68535	Adp68535 Human sec
	22	2075	46.4	2075	4	AAD17401	Aad17401 Human sec
	23	2075	46.4	2075	6	ABV73022	Abv73022 Human sec
	24	2075	46.4	2075	8	ABX75330	Abx75330 Human cDN
	25	2075	46.4	2075	8	AAD52558	Aad52558 FRP DNA.
	26	2075	46.4	2075	12	ADH43319	Adh43319 Human sec
	27	2074.6	46.4	2075	10	ADC71197	Adc71197 Human sec
	28	2059	46.1	2072	8	ABZ81830	Abz81830 Receptor
	29	1991.6	44.6	2094	8	ABZ82228	Abz82228 Human sec
	30	1256.6	28.1	1308	2	AAV19115	Aav19115 Human sec
c	31	978.6	21.9	1247	13	ACN41451	Acn41451 Human dia
	32	942	21.1	942	8	ABZ82227	Abz82227 Human sec
	33	942	21.1	942	9	ACC81035	Acc81035 Human emb
	34	899.8	20.1	942	6	ABV73023	Abv73023 Human sec
	35	899.8	20.1	942	10	ADC71198	Adc71198 ORF of th
	36	899.8	20.1	942	12	ADH43320	Adh43320 Human sec
	37	896.8	20.1	1017	10	ADC71192	Adc71192 DNA encod
	38	896.8	20.1	1017	12	ADH43314	Adh43314 Human sFR
	39	812.2	18.2	945	9	ACC81034	Acc81034 Murine em
	40	800.8	17.9	2124	2	AAV84394	Aav84394 Partial F
	41	684.2	15.3	804	10	ADC71195	Adc71195 DNA encod
	42	684.2	15.3	804	12	ADH43317	Adh43317 Human sec
	43	621.2	13.9	741	10	ADC71194	Adc71194 DNA encod
	44	621.2	13.9	741	12	ADH43316	Adh43316 Human sec
	45	609.6	13.6	1146	8	ABX75340	Abx75340 Human cDN
	46	609.6	13.6	1146	8	AAD52570	Aad52570 SRFP 1 DN
	47	609.6	13.6	1146	8	ABZ81842	Abz81842 WIF-1 nuc
	48	551.8	12.3	566	14	ACL62743	Acl62743 Human col
c	49	527	11.8	548	4	AAF17593	Aaf17593 Human bre
c	50	527	11.8	548	4	AAS47023	Aas47023 Human bre

Run on: August 3, 2006, 11:01:00 ; Search time 765 Seconds
 (without alignments)
 10930.700 Million cell updates/sec

Title: US-10-786-720-15
 Perfect score: 4469
 Sequence: 1 cctgcagcctccggagtcag.....taatcaatgaaaaaaaaaaaa 4469

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : Issued Patents_NA:*
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 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	4469	100.0	4469	3	US-09-949-016-428	Sequence 428, App
2	4469	100.0	4469	5	US-09-796-008-1	Sequence 1, Appli
3	4356.8	97.5	4500	3	US-09-087-031E-27	Sequence 27, Appl
4	3935	88.1	4245	3	US-09-276-531-16	Sequence 16, Appl
5	3258.8	72.9	7360	3	US-09-949-016-15054	Sequence 15054, A
6	3258.4	72.9	3360	3	US-09-949-016-3312	Sequence 3312, Ap
7	2075	46.4	2075	3	US-09-087-031E-2	Sequence 2, Appli
8	2075	46.4	2075	3	US-09-546-043-1	Sequence 1, Appli
9	2075	46.4	2075	3	US-09-514-885-2	Sequence 2, Appli
10	2062	46.1	2078	3	US-09-087-031E-1	Sequence 1, Appli
11	1256.6	28.1	1308	3	US-08-937-067-18	Sequence 18, Appl
12	899.8	20.1	942	3	US-09-546-043-2	Sequence 2, Appli
13	896.8	20.1	1017	3	US-09-546-043-9	Sequence 9, Appli
14	776.2	17.4	2124	3	US-09-087-031E-26	Sequence 26, Appl
15	684.2	15.3	804	3	US-09-546-043-12	Sequence 12, Appl
16	621.2	13.9	741	3	US-09-546-043-11	Sequence 11, Appl
c 17	600.6	13.4	601	3	US-09-949-016-26352	Sequence 26352, A
c 18	600.6	13.4	601	3	US-09-949-016-119368	Sequence 119368,

c	19	597.4	13.4	601	3	US-09-949-016-26353	Sequence 26353, A
c	20	597.4	13.4	601	3	US-09-949-016-119369	Sequence 119369,
c	21	587	13.1	601	3	US-09-949-016-26354	Sequence 26354, A
c	22	587	13.1	601	3	US-09-949-016-119370	Sequence 119370,
c	23	579.6	13.0	601	3	US-09-949-016-26355	Sequence 26355, A
c	24	579.6	13.0	601	3	US-09-949-016-119371	Sequence 119371,
c	25	527	11.8	548	3	US-09-222-575-78	Sequence 78, Appl
c	26	527	11.8	548	3	US-09-389-681-78	Sequence 78, Appl
c	27	527	11.8	548	3	US-09-620-405B-78	Sequence 78, Appl
c	28	527	11.8	548	3	US-09-339-338-78	Sequence 78, Appl
c	29	527	11.8	548	3	US-09-433-826B-78	Sequence 78, Appl
c	30	527	11.8	548	3	US-09-604-287A-78	Sequence 78, Appl
c	31	527	11.8	548	3	US-09-285-480-78	Sequence 78, Appl
c	32	527	11.8	548	3	US-09-834-759-78	Sequence 78, Appl
c	33	527	11.8	548	3	US-09-590-751A-78	Sequence 78, Appl
c	34	527	11.8	548	3	US-09-551-621-78	Sequence 78, Appl
c	35	527	11.8	548	3	US-09-551-621A-78	Sequence 78, Appl
c	36	527	11.8	548	3	US-10-076-622-78	Sequence 78, Appl
c	37	527	11.8	548	4	US-10-124-805-78	Sequence 78, Appl
	38	468.8	10.5	588	3	US-09-546-043-10	Sequence 10, Appl
	39	444	9.9	690	3	US-09-546-043-13	Sequence 13, Appl
	40	400	9.0	1984	3	US-08-937-067-5	Sequence 5, Appli
	41	399.2	8.9	1905	3	US-09-949-016-429	Sequence 429, App
	42	393.4	8.8	1719	3	US-09-949-016-1835	Sequence 1835, Ap
c	43	320	7.2	601	3	US-09-949-016-26356	Sequence 26356, A
c	44	320	7.2	601	3	US-09-949-016-119372	Sequence 119372,
	45	253.2	5.7	9086	3	US-09-949-016-13577	Sequence 13577, A
	46	253.2	5.7	85369	3	US-09-949-016-12171	Sequence 12171, A
	47	238.4	5.3	240	5	US-09-796-008-3	Sequence 3, Appli
	48	233.6	5.2	2030	3	US-08-937-067-1	Sequence 1, Appli
	49	224.8	5.0	2027	5	US-08-949-904A-1	Sequence 1, Appli
	50	223.4	5.0	1869	3	US-09-148-545-56	Sequence 56, Appl

Run on: August 3, 2006, 11:09:19 ; Search time 4965 Seconds
(without alignments)
11060.109 Million cell updates/sec

Title: US-10-786-720-15
Perfect score: 4469
Sequence: 1 cctgcagcctccggagtcag.....taatcaatgaaaaaaaaaaaa 4469

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	4469	100.0	4469	3	US-09-796-008-1	Sequence 1, Appli	
2	4469	100.0	4469	7	US-10-133-937-42	Sequence 42, Appl	
3	4469	100.0	4469	7	US-10-172-118-857	Sequence 857, App	
4	4469	100.0	4469	7	US-10-159-563-42	Sequence 42, Appl	
5	4469	100.0	4469	8	US-10-342-887-857	Sequence 857, App	
6	4469	100.0	4469	9	US-10-786-720-15	Sequence 15, Appl	
7	4469	100.0	4469	9	US-10-788-792-21	Sequence 21, Appl	
8	4469	100.0	4469	9	US-10-473-974-203	Sequence 203, App	
9	4469	100.0	4469	9	US-10-817-525-1	Sequence 1, Appli	
10	4469	100.0	4469	16	US-11-245-147-203	Sequence 203, App	
c 11	4439.8	99.3	4608	10	US-10-821-234-137	Sequence 137, App	
12	4393.4	98.3	4462	3	US-09-974-298-28	Sequence 28, Appl	

13	4356.8	97.5	4500	7	US-10-138-434A-27	Sequence 27, Appl
14	3102.6	69.4	3215	3	US-09-925-301-51	Sequence 51, Appl
15	2465.4	55.2	2602	8	US-10-666-851-1	Sequence 1, Appli
16	2075	46.4	2075	7	US-10-138-434A-2	Sequence 2, Appli
17	2075	46.4	2075	7	US-10-425-586-1	Sequence 1, Appli
18	2075	46.4	2075	8	US-10-466-136-1	Sequence 1, Appli
19	2062	46.1	2078	7	US-10-138-434A-1	Sequence 1, Appli
20	1991.6	44.6	2094	10	US-10-756-149-3306	Sequence 3306, Ap
21	1256.6	28.1	1308	6	US-10-146-474-18	Sequence 18, Appl
22	1256.6	28.1	1308	8	US-10-301-764-18	Sequence 18, Appl
23	899.8	20.1	942	7	US-10-425-586-2	Sequence 2, Appli
24	899.8	20.1	942	8	US-10-466-136-2	Sequence 2, Appli
25	896.8	20.1	1017	7	US-10-425-586-9	Sequence 9, Appli
26	776.2	17.4	2124	7	US-10-138-434A-26	Sequence 26, Appl
27	684.2	15.3	804	7	US-10-425-586-12	Sequence 12, Appl
28	621.2	13.9	741	7	US-10-425-586-11	Sequence 11, Appl
29	571.4	12.8	630	12	US-10-301-480-560598	Sequence 560598,
30	571.4	12.8	630	12	US-10-301-480-1174007	Sequence 1174007,
c 31	527	11.8	548	3	US-09-604-287A-78	Sequence 78, Appl
c 32	527	11.8	548	3	US-09-834-759-78	Sequence 78, Appl
c 33	527	11.8	548	3	US-09-339-338-78	Sequence 78, Appl
c 34	527	11.8	548	3	US-09-551-621-78	Sequence 78, Appl
c 35	527	11.8	548	6	US-10-007-805-78	Sequence 78, Appl
c 36	527	11.8	548	6	US-10-076-622-78	Sequence 78, Appl
c 37	527	11.8	548	7	US-10-124-805-78	Sequence 78, Appl
c 38	527	11.8	548	7	US-10-441-893-78	Sequence 78, Appl
c 39	527	11.8	548	16	US-11-226-869-78	Sequence 78, Appl
40	497	11.1	549	6	US-10-027-632-93316	Sequence 93316, A
41	497	11.1	549	6	US-10-027-632-305035	Sequence 305035,
42	497	11.1	549	7	US-10-027-632-93316	Sequence 93316, A
43	497	11.1	549	7	US-10-027-632-305035	Sequence 305035,
c 44	482	10.8	501	3	US-09-954-531-885	Sequence 885, App
c 45	482	10.8	501	3	US-09-954-531-1298	Sequence 1298, Ap
c 46	482	10.8	501	10	US-10-843-641A-1952	Sequence 1952, Ap
c 47	482	10.8	501	10	US-10-843-641A-2365	Sequence 2365, Ap
48	468.8	10.5	588	7	US-10-425-586-10	Sequence 10, Appl
49	444	9.9	690	7	US-10-425-586-13	Sequence 13, Appl
50	427.6	9.6	445	8	US-10-242-535A-43352	Sequence 43352, A

Run on: August 3, 2006, 11:00:10 ; Search time 19407 Seconds
 (without alignments)
 12876.977 Million cell updates/sec

Title: US-10-786-720-15
 Perfect score: 4469
 Sequence: 1 cctgcagcctccggagtcag.....taatcaatgaaaaaaaaaaaa 4469

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_htc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
	No.	Score	Query Match Length	DB	ID		
c	1	933.2	20.9	946	6	BC004466	BC004466 Homo sapi
	2	898	20.1	919	6	CR613872	CR613872 full-leng
	3	894.8	20.0	919	4	BX343566	BX343566 BX343566
	4	891	19.9	2704	6	AK088868	AK088868 Mus muscu
	5	887.6	19.9	918	1	AL528023	AL528023 AL528023
	6	845.6	18.9	887	4	BX402193	BX402193 BX402193
	7	821.8	18.4	911	5	CD519089	CD519089 AGENCOURT
	8	815.6	18.3	908	1	AU125245	AU125245 AU125245
	9	796.2	17.8	801	9	CX781693	CX781693 HESC3_8_B
	10	782.6	17.5	838	2	BG682306	BG682306 602629621
	11	780.8	17.5	891	8	CV810231	CV810231 AGENCOURT
	12	778.2	17.4	1011	3	BU196604	BU196604 AGENCOURT
	13	768	17.2	837	1	AU131621	AU131621 AU131621
	14	760.4	17.0	763	9	CX786676	CX786676 HESC3 63

	15	759.8	17.0	785	9	CX781701	CX781701	HESC3_8_C
	16	754.2	16.9	2298	6	AK081052	AK081052	Mus muscu
	17	748.6	16.8	782	9	DA571541	DA571541	DA571541
c	18	748.6	16.8	886	1	AL528022	AL528022	AL528022
	19	746	16.7	952	8	CO580514	CO580514	ILLUMIGEN
	20	744.4	16.7	884	2	BG681605	BG681605	602628094
	21	736.8	16.5	764	1	AU123839	AU123839	AU123839
	22	736.8	16.5	814	5	CD644680	CD644680	AGENCOURT
	23	732.8	16.4	913	3	BQ879583	BQ879583	AGENCOURT
c	24	727.8	16.3	803	5	CD616079	CD616079	56076764J
	25	725.8	16.2	878	3	BQ876624	BQ876624	AGENCOURT
	26	721.4	16.1	762	8	CN271890	CN271890	170004245
	27	720.4	16.1	898	3	BQ680787	BQ680787	AGENCOURT
	28	718.6	16.1	864	5	CD558546	CD558546	AGENCOURT
	29	715.4	16.0	750	8	CN271875	CN271875	170005313
	30	711	15.9	922	3	BQ932355	BQ932355	AGENCOURT
	31	709.8	15.9	734	8	CN271881	CN271881	170006001
	32	709.4	15.9	723	4	CA389569	CA389569	cs100d05.
	33	708.6	15.9	762	1	AU125808	AU125808	AU125808
	34	704.6	15.8	757	8	CN271867	CN271867	170005327
c	35	694.4	15.5	703	4	CA413793	CA413793	UI-H-EZ0-
c	36	693.8	15.5	701	4	CA313964	CA313964	UI-CF-FN0
c	37	689.2	15.4	701	3	BM670202	BM670202	UI-E-DW1-
	38	681	15.2	823	1	AU127052	AU127052	AU127052
	39	672.6	15.1	903	5	CD244905	CD244905	AGENCOURT
	40	667.4	14.9	792	2	BG698901	BG698901	602703318
	41	665	14.9	881	2	BG253035	BG253035	602365657
	42	664.8	14.9	779	4	CB247875	CB247875	UI-M-FI0-
	43	662.6	14.8	982	3	BU501489	BU501489	AGENCOURT
	44	661.8	14.8	741	8	CR769220	CR769220	DKFZp469B
	45	661.2	14.8	928	2	BG120117	BG120117	602353481
	46	660	14.8	779	5	CD643855	CD643855	AGENCOURT
	47	658.2	14.7	907	2	BG119546	BG119546	602347246
c	48	657.2	14.7	706	4	CA434170	CA434170	UI-H-DH0-
	49	655.4	14.7	738	3	BQ771388	BQ771388	UI-M-FI0-
c	50	654.4	14.6	660	3	BM970588	BM970588	UI-CF-EC1